

What is claimed is:

1. A method for identifying a potentially transcribed region of a genome comprising:
 - a) Hybridizing a plurality of nucleic acid probes with a nucleic acid sample, wherein said nucleic acid sample comprises transcripts from said genome, wherein said probes are targeting an area of said genome; and
 - b) Identifying said transcribed region as a region of said genome where hybridization of all consecutive probes targeting said region are above a threshold value.
- 10 2. The method of Claim 1 wherein said probes are oligonucleotides.
3. The method of Claim 2 wherein said oligonucleotides are immobilized on a substrate.
4. The method of Claim 1 wherein said threshold value is non-specific binding.
5. The method of Claim 4 wherein said non-specific binding is measured using a probe designed to contain at least one mismatched base.
- 15 6. The method of Claim 1 further comprising identifying a sub-region wherein hybridization of said probes targeting said sub-regions is similar and indicating said sub-region as said transcribed region.
7. The method of Claim 6 wherein said genome is from a prokaryote.
- 20 8. The method of Claim 7 wherein said transcribed region is an operon.
9. The method of Claim 8 wherein said prokaryote is bacteria.
10. A computer software product comprising:

- a) a computer program code that receives a plurality of hybridization intensities, wherein each of said intensities reflects the hybridization of one of a plurality of probes to a nucleic acid sample and wherein said probes are targeting a genome;
 - 5 b) a computer program code that identifies a region of said genome wherein intensities for said probes against said region are above a threshold value; and
 - c) a computer readable media for storing said codes.
11. The computer software product of Claim 10 further comprising a computer program code that identifies an area of said region wherein intensities for said probes against said area are similar.
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12. The computer software product of Claim 11 wherein the difference in said intensities for said probes against said area is within 2 fold.
13. The computer software product of Claim 12 wherein said difference is within 150%.
- 15 14. The computer software product of Claim 11 further comprising a computer program code to indicate said area as a transcribed area.